

RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/887,879

TIME: 15:12:39

Input Set : N:\Crf3\RULE60\09887879.txt

Output Set: N:\CRF3\12212001\I887879.raw

5 <110> APPLICANT: Ashkenazi, Avi J.
 7 Baker, Kevin P.
 9 Chuntharapai, Anan
 11 Gurney, Austin
 13 Kim, Kyung Jin
 15 Wood, William I.
 19 <120> TITLE OF INVENTION: Apo-2DcR
 23 <130> FILE REFERENCE: P1110P1
 25 <140> CURRENT APPLICATION NUMBER: 09/887,879
 27 <141> CURRENT FILING DATE: 2001-06-21
 29 <150> PRIOR APPLICATION NUMBER: 09/096,500
 31 <151> PRIOR FILING DATE: 1998-06-12
 35 <150> PRIOR APPLICATION NUMBER: US 60/049,911
 37 <151> PRIOR FILING DATE: 1997-06-18
 41 <160> NUMBER OF SEQ ID NOS: 17
 45 <210> SEQ ID NO: 1
 47 <211> LENGTH: 259
 49 <212> TYPE: PRT

ENTERED

51 <213> ORGANISM: Homo sapiens
 55 <400> SEQUENCE: 1
 57 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
 59 1 5 10 15
 63 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
 65 20 25 30
 69 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
 71 35 40 45
 75 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
 77 50 55 60
 81 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
 83 65 70 75
 87 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
 89 80 85 90
 93 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
 95 95 100 105
 99 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
 101 110 115 120
 105 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
 107 125 130 135
 111 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
 113 140 145 150
 117 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
 119 155 160 165
 123 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
 125 170 175 180
 129 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
 131 185 190 195
 135 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu

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```

137          200          205          210
141  Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
143          215          220          225
147  Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
149          230          235          240
153  Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
155          245          250          255
159  Ile Val Phe Val
165 <210> SEQ ID NO: 2
167 <211> LENGTH: 1180
169 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
175 <220> FEATURE:
177 <221> NAME/KEY: CDS
179 <222> LOCATION: (193) . . . (969)
181 <223> OTHER INFORMATION:
185 <400> SEQUENCE: 2
187  gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
191  atttttggga gtttgaccag agatgcaagg ggtgaaggag cgcttcctac 100
195  cgtaggggaa ctctggggac agagcgcccc ggccgcctga tggccgaggc 150
199  aggggtgcgac ccaggaccca ggacggcgtc gggaaccata cc  atg 195
201                                     Met
203                                     1
207  gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc 234
209  Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
211          5          10
215  gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc 273
217  Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
219  15          20          25
223  act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 312
225  Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
227          30          35          40
231  cca cag caa cag agg cac agc ttc aag ggg gag gag tgt 351
233  Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
235          45          50
239  cca gca gga tct cat aga tca gaa cat act gga gcc tgt 390
241  Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
243          55          60          65
247  aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 429
249  Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
251          70          75
255  aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa 468
257  Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
259  80          85          90
263  tca gat caa aaa cat aaa agt tcc tgc acc atg acc aga 507
265  Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
267          95          100          105
271  gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat 546
273  Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn

```

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```

275          110          115
279 gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc 585
281 Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
283      120          125      130
287 cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc tgg 624
289 Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
291          135          140
295 gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc 663
297 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
299 145          150          155
303 act gtg gaa acc cca gct gct gaa gag aca atg aac acc 702
305 Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
307      160          165      170
311 agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 741
313 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
315          175          180
319 aac acc agc cca ggg act cct gcc cca gct gct gaa gag 780
321 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
323 185          190          195
327 aca atg acc acc agc ccg ggg act cct gcc cca gct gct 819
329 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
331          200          205
335 gaa gag aca atg acc acc agc ccg ggg act cct gcc cca 858
337 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
339 210          215          220
343 gct gct gaa gag aca atg acc acc agc ccg ggg act cct 897
345 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
347      225          230          235
351 gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 936
353 Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
355          240          245
359 ata gtt cta att gtg ctt ctg att gtg ttt gtt t 970
361 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
W--> 363      250          255          259
367 gaaagacttc actgtggaag aaattccttc cttacctgaa aggttcaggt 1020
371 aggcgctggc tgagggcggg gggcgctgga cactctctgc cctgcctccc 1070
375 tctgctgtgt tcccacagac agaaacgcct gccctgccc caaaaaaaaa 1120
379 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1170
383 aaaaaaaaaa 1180
387 <210> SEQ ID NO: 3
389 <211> LENGTH: 299
391 <212> TYPE: PRT
393 <213> ORGANISM: Homo sapiens
397 <400> SEQUENCE: 3
399 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
401 1          5          10          15
405 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
407          20          25          30
411 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro

```

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```

413          35          40          45
417  Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
419          50          55          60
423  Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
425          65          70          75
429  Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
431          80          85          90
435  Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
437          95         100         105
441  Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
443         110         115         120
447  Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
449         125         130         135
453  Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
455         140         145         150
459  Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
461         155         160         165
465  Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn
467         170         175         180
471  Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala
473         185         190         195
477  Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
479         200         205         210
483  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr
485         215         220         225
489  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
491         230         235         240
495  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
497         245         250         255
501  Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr
503         260         265         270
507  Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile
509         275         280         285
513  Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
515         290         295
519 <210> SEQ ID NO: 4
521 <211> LENGTH: 1180
523 <212> TYPE: DNA
525 <213> ORGANISM: Homo sapiens
529 <220> FEATURE:
531 <221> NAME/KEY: CDS
533 <222> LOCATION: (73) . . . (969)
535 <223> OTHER INFORMATION:
539 <220> FEATURE:
541 <221> NAME/KEY: sig_peptide
543 <222> LOCATION: (73) . . . (194)
545 <223> OTHER INFORMATION:
549 <400> SEQUENCE: 4
551  gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50

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```

555 atttttggga gtttgaccag ag      atg caa ggg gtg aag gag 90
557                               Met Gln Gly Val Lys Glu
559                               -40                               -35
563 cgc ttc cta ccg tta ggg aac tct ggg gac aga gcg ccc 129
565 Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
567                               -30                               -25
571 cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 168
573 Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
575                               -20                               -15                               -10
579 cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc 207
581 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
583                               -5                               1                               5
587 aag acc cta aag ttc gtc gtc gtc atc gtc gcg gtc ctg 246
589 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
591                               10                               15
595 ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 285
597 Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
599                               20                               25                               30
603 gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag 324
605 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
607                               35                               40
611 agg cac agc ttc aag ggg gag gag tgt cca gca gga tct 363
613 Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
615                               45                               50                               55
619 cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca 402
621 His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
623                               60                               65                               70
627 gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct 441
629 Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
631                               75                               80
635 tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa aaa 480
637 Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
639                               85                               90                               95
643 cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt 519
645 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
647                               100                              105
651 cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca 558
653 Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
655                               110                              115                              120
659 gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa 597
661 Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
663                               125                              130                              135
667 gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag 636
669 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
671                               140                              145
675 tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc 675
677 Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
679                               150                              155                              160
683 cca gct gct gaa gag aca atg aac acc agc ccg ggg act 714

```

VERIFICATION SUMMARY

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DATE: 12/21/2001

TIME: 15:12:40

Input Set : N:\Crf3\RULE60\09887879.txt

Output Set: N:\CRF3\12212001\I887879.raw

L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:743 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:1247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11